GenCore version 5.1.6


OM nucleic - protein search, using frame_plus_n2p model

Run on: August 22, 2003, 13:47:31 ; Search time 103 Seconds
(without alignments)
4786.454 Million cell updates/sec

Title: US-09-745-506-74
Perfect score: 2789
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1890 | 67.8 | 377 | 22 | AAU27744 | Human full-length |
| 3 | 1799 | 64.5 | 350 | 22 | AAG81361 | Human AFP protein |
| 4 | 1799 | 64.5 | 350 | 22 | AAB94573 | Human protein sequ |
| 5 | 1743.5 | 62.5 | 351 | 22 | AAB60663 | Human gene express |
| 6 | 1209 | 43.3 | 247 | 23 | ABB08182 | Human protein kina |
| 7 | 599 | 21.5 | 146 | 22 | AAU27916 | Human contig polyp |
| 8 | 578 | 20.7 | 288 | 22 | ABB60530 | Drosophila melanog |
| 9 | 518 | 18.6 | 110 | 22 | ABG20985 | Novel human diagno |
| 10 | 366 | 13.1 | 68 | 22 | ABG52473 | Human liver peptid |
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| 13 | 366 | 13.1 | 68 | 22 | AAM58295 | Human brain expres |
| 14 | 366 | 13.1 | 68 | 22 | AAM18609 | Peptide #5043 enco |
| 15 | 366 | 13.1 | 68 | 22 | AAM06178 | Peptide #4860 enco |
| 16 | 330 | 11.8 | 79 | 22 | AAU21467 | Human novel foetal |
| 17 | 314.5 | 11.3 | 70 | 22 | ABG20982 | Novel human diagno |
| 18 | 305 | 10.9 | 367 | 23 | ABP38833 | Staphylococcus epi |
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| 20 | 289.5 | 10.4 | 403 | 22 | AAU54649 | Propionibacterium |
| 21 | 249 | 8.9 | 376 | 22 | AAG82506 | S. epidermidis ope |
| 22 | 240 | 8.6 | 373 | 23 | ABB47970 | Listeria monocytog |
| 23 | 230 | 8.2 | 380 | 22 | AAG92198 | C glutamicum prote |
| 24 | 230 | 8.2 | 380 | 22 | AAB79495 | Corynebacterium gl |
| 25 | 216.5 | 7.8 | 379 | 24 | ABP57497 | Mycobacterium tube |
| 26 | 216 | 7.7 | 264 | 23 | ABP26738 | Streptococcus poly |
| 27 | 203.5 | 7.3 | 265 | 24 | ABU02074 | S. pneumoniae type |
| 28 | 190 | 6.8 | 58 | 22 | AAM90790 | Human immune/haema |
| 29 | 187.5 | 6.7 | 256 | 23 | ABB54389 | Lactococcus lactis |
| 30 | 174 | 6.2 | 262 | 23 | ABP30359 | Streptococcus poly |
| 31 | 174 | 6.2 | 263 | 23 | ABP26737 | Streptococcus poly |
| 32 | 157.5 | 5.6 | 244 | 22 | AAG81950 | S. epidermidis ope |
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| 34 | 120 | 4.3 | 316 | 23 | AAM49408 | Escherichia coli r |
| c 35 | 115 | 4.2 | 22 | 22 | ABG20983 | Novel human diagno |
| 36 | 109.5 | 3.9 | 733 | 22 | AAU18289 | Human endocrine po |
| c 37 | 107 | 3.9 | 961 | 23 | AAU80188 | Human TSP1 domain |
| c 38 | 107 | 3.9 | 966 | 23 | AAU80189 | Human TSP1 domain |
| 39 | 105.5 | 3.8 | 3829 | 22 | AAB97819 | Human spastin prot |
| 40 | 105.5 | 3.8 | 3829 | 22 | AAB97823 | Human mutated spas |
| 41 | 105 | 3.8 | 644 | 14 | AAR38751 | DEL protein. Anti |
| 42 | 104.5 | 3.7 | 473 | 23 | ABG61562 | High growth methan |
| 43 | 104.5 | 3.7 | 473 | 23 | AAU79436 | Methylomonas glyco |
| 44 | 103.5 | 3.7 | 3830 | 22 | AAB97820 | Mouse spastin prot |
| 45 | 103 | 3.7 | 673 | 20 | AAW93593 | Human kidney amino |

ALIGNMENTS

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DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen SEQ ID NO:15678.
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KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR N-PSDB; AAK60866.

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PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and
PT   metastasis -
XX
PS   Claim 11; SEQ ID NO 15678; 3071pp + Sequence Listing; English.
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
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SQ   Sequence   383 AA;

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Query Match:            67.98%         Indels:          0
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RESULT 2
AAU27744
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AC   AAU27744;
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DT   18-DEC-2001  (first entry)
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DE   Human full-length polypeptide sequence #69.
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KW   Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW   mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW   cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW   nervous system disorder; inflammatory disorder; cell differentiation;
KW   angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW   genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW   cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory;
KW   antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW   neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
KW   immunostimulant; analgesic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200164834-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04926.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
PR   17-JUN-2000; 2000US-0597707.
PR   14-JUL-2000; 2000US-0616807.
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PR 19-SEP-2000; 2000US-0664641.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Drmanac R;
XX
DR WPI; 2001-589862/66.
DR N-PSDB; AAS44644.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of
PT cancer, neurological, inflammatory disorders and for use in arrays for
PT detection -
XX
PS Claim 10; SEQ ID No 241; 153pp; English.
XX
CC Sequences AAU27676-AAU28019 represent full-length polypeptides and
CC contig polypeptides of the invention. The proteins and their associated
CC DNA sequences are useful for the treatment, diagnosis and prevention of
CC various types of disorder in a mammalian subject such as a human, dog,
CC monkey, mouse, hamster or rat. The disorders include cancers such as
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 377 AA;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 2.6e-180 | Length: | 377 |
| Score: | 1890.00 | Matches: | 369 |
| Percent Similarity: | 99.46% | Conservative: | 0 |
| Best Local Similarity: | 99.46% | Mismatches: | 2 |
| Query Match: | 67.77% | Indels: | 0 |
| DB: | 22 | Gaps: | 0 |

US-09-745-506-74 (1-1553) x AAU27744 (1-377)

```
Qy      182 AGATGAGTCCCCACGACAGTCCGGTTTGTAGATTCCCTGATCTGCAATTCTTCCCGTTCC 241
            |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        7 ArgProValProThrThrValArgPheValAspSerLeuIleCysAsnSerSerArgSer 26

Qy      242 TTCATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCT 301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       27 PheMetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAla 46

Qy      302 GAGAGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACA 361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       47 GluSerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThr 66

Qy      362 CTCTTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCA 421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       67 LeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAla 86

Qy      422 GACCTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAAC 481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 AspLeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsn 106

Qy      482 ACATGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCT 541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      107 ThrTrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerPro 126

Qy      542 CATACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGA 601
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      127 HisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 146

Qy      602 GCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAAC 661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsn 166

Qy      662 CACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTG 721
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      167 HisArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaVal 186

Qy      722 AAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAA 781
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      187 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGln 206

Qy      782 ACACGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCC 841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      207 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 226

Qy      842 CGGAACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTA 901
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      227 ArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeu 246

Qy      902 CATACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATT 961
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      247 HisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIle 266

Qy      962 GATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGA 1021
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      267 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 286

Qy     1022 ACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTG 1081
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      287 ThrLeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeu 306

Qy     1082 CAGGGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGAT 1141
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      307 GlnGlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspIleLeuAsp 326

Qy     1142 GCTGCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTT 1201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      327 AlaAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPhe 346

Qy     1202 CTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTA 1261
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      347 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeu 366

Qy     1262 TCAGAGACTGACAGGGACCCTCTTCAGGTGGTA 1294
            |||||||||||||||||||||||||||||||||
Db      367 SerGluThrAspArgAspProLeuGlnValVal 377
```

RESULT 3
AAG81361
ID AAG81361 standard; Protein; 350 AA.
XX
AC AAG81361;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human AFP protein sequence SEQ ID NO:240.
XX
KW Human; secreted protein; secretion; bacterial cell; fungal cell;
KW eukaryotic cell; fusion protein; maltose binding protein;
KW immunoglobulin constant region; polyhistidine tag.
XX
OS Homo sapiens.
XX
PN WO200129221-A2.

```
XX
PD   26-APR-2001.
XX
PF   20-OCT-2000; 2000WO-US29052.
XX
PR   20-OCT-1999;   99US-0160712.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Conklin DC,  Yee DP;
XX
DR   WPI; 2001-300340/31.
DR   N-PSDB; AAH52212.
XX
PT   Isolated polypeptide for directing secretion of proteins of interest
PT   from a host cell including, e.g. bacteria, includes contiguous amino
PT   acid residues of polypeptide with specified amino acids
XX
PS   Claim 1; Page 424-425; 617pp; English.
XX
CC   AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242
CC   to AAG81453. The secreted proteins can be used for directing the
CC   secretion of proteins of interest from a host cell including bacteria,
CC   fungal cells, and cultured higher eukaryotic cells. The present invention
CC   also describes fusion proteins, where a secreted protein of the invention
CC   is operably linked via a peptide bond or peptide linker to a second
CC   protein selected from the group consisting of maltose binding protein,
CC   an immunoglobulin constant region, a polyhistidine tag and a peptide
CC   given in AAG81453.
XX
SQ   Sequence   350 AA;

Alignment Scores:
Pred. No.:              3.36e-171      Length:          350
Score:                  1799.00        Matches:         350
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            64.50%         Indels:          0
DB:                     22             Gaps:            0

US-09-745-506-74 (1-1553) x AAG81361 (1-350)

Qy        245 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20

Qy        305 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40

Qy        365 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60

Qy        425 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80

Qy        485 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100

Qy        545 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120

Qy        605 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140

Qy        665 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160

Qy        725 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180

Qy        785 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200

Qy        845 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220

Qy        905 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240

Qy        965 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1024
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260

Qy       1025 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1084
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280

Qy       1085 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300

Qy       1145 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320

Qy       1205 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340

Qy       1265 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1294
              |||||||||||||||||||||||||||||
Db        341 GluThrAspArgAspProLeuGlnValVal 350

RESULT 4
AAB94573
ID   AAB94573 standard; Protein; 350 AA.
XX
AC   AAB94573;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human protein sequence SEQ ID NO:15360.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
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XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 15360; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence   350 AA;

Alignment Scores:
Pred. No.:                3.36e-171      Length:          350
Score:                    1799.00        Matches:         350
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              64.50%         Indels:          0
DB:                       22             Gaps:            0

US-09-745-506-74 (1-1553) x AAB94573 (1-350)

Qy        245 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20

Qy        305 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40

Qy        365 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60

Qy        425 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80

Qy        485 TGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCAT 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100

Qy        545 ACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120

Qy        605 TGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140

Qy        665 CGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAA 724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160

Qy        725 GGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACA 784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180

Qy        785 CGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGG 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200

Qy        845 AACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACAT 904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220

Qy        905 ACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGAT 964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240

Qy        965 CGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACC 1024
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260

Qy       1025 TTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAG 1084
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280

Qy       1085 GGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCT 1144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300

Qy       1145 GCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTT 1204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320

Qy       1205 TCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCA 1264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSer 340

Qy       1265 GAGACTGACAGGGACCCTCTTCAGGTGGTA 1294
              |||||||||||||||||||||||||||||
Db        341 GluThrAspArgAspProLeuGlnValVal 350

RESULT 5
AAB60663
ID   AAB60663 standard; Protein; 351 AA.
XX
AC   AAB60663;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human gene expression regulatory factor-related protein hNIF3-s.
XX
KW   Human gene expression regulatory factor-related protein; hNIF3-s;
KW   NGG1-interacting factor; haemopoietic stem cell; preparation;
KW   detection.
XX
OS   Homo sapiens.
XX
PN   CN1272543-A.
XX
PD   08-NOV-2000.
XX
PF   11-APR-2000; 2000CN-0115369.
XX
PR   11-APR-2000; 2000CN-0115369.
XX
PA   (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI   Li N,  Xiao H,  Liu F;
XX
DR   WPI; 2001-183596/19.
DR   N-PSDB; AAF59945.
XX
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PT   Human gene expression regulatory factor related protein and its coded
PT   sequence -
XX
PS   Claim 4; Page 19-20; 20pp; Chinese.
XX
CC   The invention relates to a novel human gene expression regulatory
CC   factor-related protein, hNIF3-s (NGG1-interacting factor, AAB60663),
CC   and cDNA encoding it (AAF59945). hNIF3-s is expressed in haemopoietic
CC   stem cells. The invention also relates to the preparation of hNIF3-s
CC   proteins and nucleic acids, and the detection of hNIF3-s proteins and
CC   nucleic acids in a sample. The present sequence represents hNIF3-s.
XX
SQ   Sequence   351 AA;

Alignment Scores:
Pred. No.:              1.25e-165      Length:          351
Score:                  1743.50        Matches:         344
Percent Similarity:     98.58%         Conservative:    2
Best Local Similarity:  98.01%         Mismatches:      4
Query Match:            62.51%         Indels:          1
DB:                     22             Gaps:            1

US-09-745-506-74 (1-1553) x AAB60663 (1-351)

Qy        245 ATGGATTTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20

Qy        305 AGTTGGGACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTC 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 SerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40

Qy        365 TTCCTGACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGAC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60

Qy        425 CTCATTCTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGG---AAC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   :::
Db         61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleAsnLeuGluHis 80

Qy        482 ACATGGAAGGAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCT 541
                 :::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 MetGlyArgGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerPro 100

Qy        542 CATACAGCCTATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 HisThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 120

Qy        602 GCTTGTACCTCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAAC 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsn 140

Qy        662 CACCGAGTAGAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTG 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 HisArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaVal 160

Qy        722 AAAGGAATTGACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAA 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGln 180

Qy        782 ACACGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCC 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 200

Qy        842 CGGAACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTA 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeu 220

Qy        902 CATACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATT 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 HisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIle 240

Qy        962 GATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGA 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg 260

Qy       1022 ACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ThrLeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeu 280

Qy       1082 CAGGGTGTTGAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGAT 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GlnGlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAsp 300

Qy       1142 GCTGCTTCCCAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AlaAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPhe 320

Qy       1202 CTTTCTGACCTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTA 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeu 340

Qy       1262 TCAGAGACTGACAGGGACCCTCTTCAGGTGGTA 1294
              ||||||||||||||||||||||||||||||||
Db        341 SerGluThrAspArgAspProLeuGlnValVal 351

RESULT 6
ABB08182
ID   ABB08182 standard; Protein; 247 AA.
XX
AC   ABB08182;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human protein kinase C 27.17 polypeptide.
XX
KW   Human; protein kinase C 27.17; protein metabolism; enzyme.
XX
OS   Homo sapiens.
XX
PN   CN1333355-A.
XX
PD   30-JAN-2002.
XX
PF   07-JUL-2000; 2000CN-0117049.
XX
PR   07-JUL-2000; 2000CN-0117049.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305609/35.
DR   N-PSDB; ABL60919.
XX
PT   Human protein kinase C 27.17 polypeptide and its encoding
PT   polynucleotide, for treating e.g. protein metabolism disturbance -
XX
PS   Claim 1; Page 26-27 (disclosure); 33pp; Chinese.
XX
CC   The invention relates to a human protein kinase C 27.17 polypeptide and
CC   its encoding polynucleotide. The polypeptide can be expressed by standard
CC   DNA recombination. The polynucleotide, polypeptide and its antagonist are
CC   useful for treating e.g. protein metabolism disturbance. The present
CC   sequence represents the human protein kinase C 27.17 polypeptide.
XX
SQ   Sequence   247 AA;

Alignment Scores:
Pred. No.:              4.32e-112      Length:          247
Score:                  1209.00        Matches:         243
Percent Similarity:     97.99%         Conservative:    1
Best Local Similarity:  97.59%         Mismatches:      3
Query Match:            43.35%         Indels:          2
DB:                     23             Gaps:            0
```

US-09-745-506-74 (1-1553) x ABB08182 (1-247)

```
Qy        552 ATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCTTGTACCT 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetMetLeuArgProArgAlaSerThrThrGlyTrpLeuLysGlyLeuGluLeuValPro 20

Qy        612 CCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCACCGAGTAG 671
              |||||| |||||||||||||| |||||||||:::|||      |||   ||||||||||
Db         21 ProGly-HisThrSerPheGln-AlaProAsnPheProTyrArgGlyThrHisArgValG 40

Qy        672 AATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAAGGAATTG 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 luPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIleA 60

Qy        732 ACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACACGGATTA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 spGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIleA 80

Qy        792 ATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGGAACAAAC 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 snLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLysG 100

Qy        852 AACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACATACTGGAA 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 lnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHisThrGlyM 120

Qy        912 TGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGATCGAATAA 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 etGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIleL 140

Qy        972 AAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACCTTAGAGT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGluS 160

Qy       1032 CTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAGGGTGTTG 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 erGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGlnGlyValG 180

Qy       1092 AGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCTGCTTCCC 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 luAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAlaAlaSerG 200

Qy       1152 AAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTTTCTGACC 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 lnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeuSerAspL 220

Qy       1212 TTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCAGAGACTG 1271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 euArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSerGluThrA 240

Qy       1272 ACAGGGACCCTCTTCAGGTGGTA 1294
              |||||||||||||||||||||||
Db        240 spArgAspProLeuGlnValVal 247
```

RESULT 7
AAU27916
ID AAU27916 standard; Protein; 146 AA.
XX
AC AAU27916;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human contig polypeptide sequence #69.
XX
KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200164834-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04926.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.
PR 19-SEP-2000; 2000US-0664641.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Drmanac R;
XX
DR WPI; 2001-589862/66.
DR N-PSDB; AAS44816.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of
PT cancer, neurological, inflammatory disorders and for use in arrays for
PT detection -
XX
PS Claim 10; Page 132; 153pp; English.
XX
CC Sequences AAU27676-AAU28019 represent full-length polypeptides and
CC contig polypeptides of the invention. The proteins and their associated
CC DNA sequences are useful for the treatment, diagnosis and prevention of
CC various types of disorder in a mammalian subject such as a human, dog,
CC monkey, mouse, hamster or rat. The disorders include cancers such as
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 146 AA;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 5.1e-51 | Length: | 146 |
| Score: | 599.00 | Matches: | 114 |
| Percent Similarity: | 94.53% | Conservative: | 7 |
| Best Local Similarity: | 89.06% | Mismatches: | 7 |
| Query Match: | 21.48% | Indels: | 0 |
| DB: | 22 | Gaps: | 0 |

US-09-745-506-74 (1-1553) x AAU27916 (1-146)

```
Qy        206 TTTGTAGATTCCCTGATCTGCAATTCTTCCCGTTCCTTCATGGATTTGAAGGCTCTCCTT 265
              ||||||||||||||||||||||||||||||||:::|||||||||   :::|||||||||
Db         19 PheValAspSerLeuIleCysAsnSerSerArgAlaPheMetAspTrpArgAlaLeuLeu 38

Qy        266 TCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAGAGTTGGGACAATGTTGGATTA 325
```

```
Db         39 SerSerLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTrpAspAsnValGlyLeu 58

Qy        326 CTGGTGGAACCAAGCCCACCACATACTGTAAATACACTCTTCCTGACCAATGACCTGACT 385

Db         59 LeuValGluProSerProProHisThrValAsnThrLeuPheLeuThrAsnAspLeuThr 78

Qy        386 GAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCG 445

Db         79 AspGluValMetAspGluValLeuLeuLysLysAlaHisLeuIleLeuSerTyrHisPro 98

Qy        446 CCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATC 505

Db         99 SerIlePheArgProMetLysArgIleThrTrpAsnThrTrpLysGluLeuLeuValIle 118

Qy        506 CGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCC 565

Db        119 ArgAlaLeuGluAsnArgValGlyIleTyrSerProTyrThrThr***GluAlaAlaPro 138

Qy        566 CAGGGCGTCAACAACTGGTTGGCT 589

Db        139 GlnGlyValAsnAsnTrpValAla 146

RESULT 8
ABB60530
ID   ABB60530 standard; Protein; 288 AA.
XX
AC   ABB60530;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 8382.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL04633.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 8382; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   288 AA;
```

```
Alignment Scores:
Pred. No.:              9.52e-49      Length:          288
Score:                  578.00        Matches:         118
Percent Similarity:     51.44%        Conservative:    61
Best Local Similarity:  33.91%        Mismatches:      81
Query Match:            20.72%        Indels:          88
DB:                     22            Gaps:            4

US-09-745-506-74 (1-1553) x ABB60530 (1-288)

Qy        251 TTGAAGGCTCTCCTTTCTTCCTTGAATGACTTTGCATCCCTCTCGTTTGCTGAGAGTTGG 310

Db          9 LeuAlaAlaValValLysGluLeuGluAsnPheAlaProThrSerTrpAlaGluLysTrp 28

Qy        311 GACAATGTTGGATTACTGGTGGAACCAAGCCCACCACATACTGTAAATACACTCTTCCTG 370

Db         29 AspAsnValGlyLeuLeuIleGluProHisArgGluLysGlnIleLysLysIleLeuLeu 48

Qy        371 ACCAATGACCTGACTGAGGAAGTGATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATT 430

Db         49 ThrAsnAspLeuThrGluProValValLysGluAlaLeuGluLysGluAlaGluLeuIle 68

Qy        431 CTCTCCTACCATCCGCCTATCTTCCGACCCATGAAGCGCATAACCTGGAACACATGGAAG 490

Db         69 IleSerTyrHisProProIlePheLysProLeuThrArgIleThrGlnSerHisTrpLys 88

Qy        491 GAGCGCCTGGTGATCCGGGCTCTGGAGAACAGAGTCGGTATCTACTCTCCTCATACAGCC 550

Db         89 GluArgValValAlaAlaCysLeuAlaAsnAspIleAlaLeuTyrSerProHisThrAla 108

Qy        551 TATGATGCTGCGCCCCAGGGCGTCAACAACTGGTTGGCTAAAGGGCTTGGAGCTTGTACC 610

Db        109 TrpAspLysLysSerGlyGlyValAsnAspTrpLeuSerLysAlaValAsnIleIleSer 128

Qy        611 TCCAGGCCCATACATCCTTCCAAAGCTCCCAACTACCCTACAGAGGGAAACCACCGAGTA 670

Db        129 IleArgProLeuGluProGlu---------------------------------------- 135

Qy        671 GAATTCAACGTTAACTACACCCAAGACCTGGACAAAGTCATGTCTGCAGTGAAAGGAATT 730

Db        136 ----------------------------------------LeuGlyAlaProProGly--- 141

Qy        731 GACGGTGTTTCTGTCACTTCTTTTTCTGCTAGGACTGGTAATGAGGAACAAACACGGATT 790

Db        141 ------------------------------------------------------------ 141

Qy        791 AATCTGAATTGTACTCAGAAGGCTTTGATGCAGGTGGTAGATTTTCTTTCCCGGAACAAA 850

Db        141 ------------------------------------------------------------ 141

Qy        851 CAACTTTATCAGAAGACGGAAATTCTGTCACTGGAGAAGCCTTTGCTTCTACATACTGGA 910

Db        142 ------------------------------------------------------ThrGly 143

Qy        911 ATGGGACGGTTATGCACACTGGATGAATCTGTCTCCCTGGCAACCATGATTGATCGAATA 970

Db        144 SerGlyArgTyr------IleGluThrLysMetGluLeuSerGlnValValGluSerLeu 161

Qy        971 AAAAGACACCTAAAACTATCTCATATTCGCTTAGCCCTTGGGGTGGGGAGAACCTTAGAG 1030

Db        162 GlnLysArgIleArgAsnSer---ValHisValAlaLeuAlaValGlyHisThrProLys 180

Qy       1031 TCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGTTCTGGGAGCAGCGTTCTGCAGGGTGTT 1090

Db        181 ThrLeuIleGlnSerValGlyIleCysAlaGlySerGlyAlaSerLeuLeuLysGlyIle 200

Qy       1091 GAGGCTGACCTTTACCTCACAGGTGAGATGTCCCATCATGATACTTTGGATGCTGCTTCC 1150

Db        201 GlnAlaAspLeuIleIleThrGlyGluMetSerHisHisGluValLeuGluPheThrHis 220

Qy       1151 CAAGGAATAAATGTCATCCTCTGTGAACACAGCAACACTGAACGAGGCTTTCTTTCTGAC 1210
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```
Db        221 AsnAsnThrThrValLeuLeuCysAsnHisSerAsnSerGluArgGlyPheLeuHisGlu 240

Qy       1211 CTTCGAGATATGCTGGATTCTCACTTGGAGAATAAGATAAATATTATCCTATCAGAGACT 1270
                 :::|||       |||      :::      :::   :::|||||
Db        241 PheCysProIleLeuAlaLysSerLeuAsnGluGluCysLeuValPheValSerGluVal 260

Qy       1271 GACAGGGACCCTCTTCAGGTGGTA 1294
              |||:::|||||||||      |||
Db        261 AspLysAspProLeuValThrVal 268

RESULT 9
ABG20985
ID   ABG20985 standard; Protein; 110 AA.
XX
AC   ABG20985;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #20976.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS85172.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 51344; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   110 AA;

Alignment Scores:

Pred. No.:              5.82e-43        Length:         110
Score:                  518.00          Matches:        108
Percent Similarity:     99.08%          Conservative:   0
Best Local Similarity:  99.08%          Mismatches:     1
Query Match:            18.57%          Indels:         1
DB:                     22              Gaps:           0

US-09-745-506-74 (1-1553) x ABG20985 (1-110)

Qy        764 ACTGGTAATGAGGAACAAACACGGATTAATCTGAATTGTACTCAGAAGGCTTTGATGCAG 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ThrGlyAsnGluGluGlnThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGln 21

Qy        824 GTGGTAGATTTTCTTTCCCGGAACAAACAACTTTATCAGAAGACGGAAATTCTGTCACTG 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 ValValAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeu 41

Qy        884 GAGAAGCCTTTGCTTCTACATACTGGAATGGGACGGTTATGCACACTGGATGAATCTGTC 943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 GluLysProLeuLeuLeuHisThrGlyMetGlyArgLeuCysThrLeuAspGluSerVal 61

Qy        944 TCCCTGGCAACCATGATTGATCGAATAAAAAGACACCTAAAACTATCTCATATTCGCTTA 1003
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 SerLeuAlaThrMetIleAspArgIleLysArgHisLeuLysLeuSerHisIleArgLeu 81

Qy       1004 GCCCTTGGGGTGGGGAGAACCTTAGAGTCTCAAGTCAAAGTCGTGGCCCTGTGTGCTGGT 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AlaLeuGlyValGlyArgThrLeuGluSerGlnValLysValValAlaLeuCysAlaGly 101

Qy       1064 TCTGGGAG-CAGCGTTCTGCAGGGTGT 1089
              ||||||   ||||||||||||||||||
Db        102 SerGlyGluGlnArgSerAlaGlyCys 110

RESULT 10
ABG52473
ID   ABG52473 standard; Peptide; 68 AA.
XX
AC   ABG52473;
XX
DT   25-FEB-2003  (first entry)
XX
DE   Human liver peptide, SEQ ID No 31121.
XX
KW   Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW   hypercholesterolaemia; coronary heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157273-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00664.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488898/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analysing gene expression in human adult liver -
XX
PS   Claim 27; SEQ ID No 31121; 658pp; English.
XX
```

```
CC   The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC   measuring human gene expression in a sample derived from human adult
CC   liver, comprising one of 13109 defined nucleotide sequences given in the
CC   specification (or complements/ fragments). The probe hybridises at high
CC   stringency to a nucleic acid molecule expressed in the human adult
CC   liver. (I) may be used for predicting, measuring and displaying gene
CC   expression in samples derived from human adult liver. The genes
CC   identified may be involved in genetic liver diseases such as cirrhosis,
CC   hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC   is associated with coronary heart disease. ABG47348-ABG59930 represent
CC   human liver single exon encoded peptides of the invention.
CC   Note: The sequence information for this patent does not appear in the
CC   printed specification but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;

Alignment Scores:
Pred. No.:              7.91e-28      Length:         68
Score:                  366.00        Matches:        68
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            13.12%        Indels:         0
DB:                     22            Gaps:           0

US-09-745-506-74 (1-1553) x ABG52473 (1-68)

Qy        395 ATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProIlePhe 20

Qy        455 CGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATCCGGGCTCTG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

Qy        515 GAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTC 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal 60

Qy        575 AACAACTGGTTGGCTAAAGGGCTT 598
              ||||||||||||||||||||||||
Db         61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 11
ABB32385
ID   ABB32385 standard; Peptide; 68 AA.
XX
AC   ABB32385;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Peptide #5036 encoded by breast cell single exon nucleic acid probe.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00662.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes  -
XX
PS   Claim 27; SEQ ID NO 15353; 327pp + sequence listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a peptide encoded by a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;

Alignment Scores:
Pred. No.:              7.91e-28      Length:         68
Score:                  366.00        Matches:        68
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            13.12%        Indels:         0
DB:                     22            Gaps:           0

US-09-745-506-74 (1-1553) x ABB32385 (1-68)

Qy        395 ATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProIlePhe 20

Qy        455 CGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATCCGGGCTCTG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

Qy        515 GAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTC 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal 60

Qy        575 AACAACTGGTTGGCTAAAGGGCTT 598
              ||||||||||||||||||||||||
Db         61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 12
ABB37667
ID   ABB37667 standard; Peptide; 68 AA.
XX
AC   ABB37667;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #5173 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
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```
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 27; SEQ ID NO 30302; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a peptide encoded by a single exon
CC   nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;

Alignment Scores:
Pred. No.:              7.91e-28        Length:         68
Score:                  366.00          Matches:        68
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            13.12%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-74 (1-1553) x ABB37667 (1-68)

Qy        395 ATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProIlePhe 20

Qy        455 CGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATCCGGGCTCTG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

Qy        515 GAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTC 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal 60

Qy        575 AACAACTGGTTGGCTAAAGGGCTT 598
              ||||||||||||||||||||||||
Db         61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 13
AAM58295
ID   AAM58295 standard; Protein; 68 AA.
XX
AC   AAM58295;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 30400.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 30400; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is a protein encoded by one of
CC   the probes of the invention.
XX
SQ   Sequence   68 AA;

Alignment Scores:
Pred. No.:              7.91e-28        Length:         68
Score:                  366.00          Matches:        68
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            13.12%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-74 (1-1553) x AAM58295 (1-68)

Qy        395 ATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProIlePhe 20

Qy        455 CGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATCCGGGCTCTG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

Qy        515 GAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTC 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal 60

Qy        575 AACAACTGGTTGGCTAAAGGGCTT 598
              ||||||||||||||||||||||||
Db         61 AsnAsnTrpLeuAlaLysGlyLeu 68

RESULT 14
AAM18609
ID   AAM18609 standard; Protein; 68 AA.
XX
AC   AAM18609;
XX
```

```
DT   12-OCT-2001  (first entry)
XX
DE   Peptide #5043 encoded by probe for measuring cervical gene expression.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 27; SEQ ID No 23435; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC   by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC   can be used to produce a single exon microarray, which can be used for
CC   measuring human gene expression in a sample derived from human cervical
CC   epithelial cells. By measuring gene expression, the probes are therefore
CC   useful in grading and/or staging of diseases of the cervix, notably
CC   cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;

Alignment Scores:
Pred. No.:              7.91e-28        Length:         68
Score:                  366.00          Matches:        68
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            13.12%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-74 (1-1553) x AAM18609 (1-68)

Qy        395 ATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProIlePhe 20

Qy        455 CGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATCCGGGCTCTG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

Qy        515 GAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTC 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal 60

Qy        575 AACAACTGGTTGGCTAAAGGGCTT 598
              ||||||||||||||||||||||||
Db         61 AsnAsnTrpLeuAlaLysGlyLeu 68
```

```
RESULT 15
AAM06178
ID   AAM06178 standard; Protein; 68 AA.
XX
AC   AAM06178;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Peptide #4860 encoded by probe for measuring breast gene expression.
XX
KW   Probe; human; breast disease; breast cancer; development disorder;
KW   inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS   Homo sapiens.
XX
PN   WO200157270-A2.
XX
PD   09-AUG-2001.
XX
PF   29-JAN-2001; 2001WO-US00661.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-476286/51.
XX
PT   Novel single exon nucleic acid probe used to measuring gene expression
PT   in a human breast -
XX
PS   Claim 27; SEQ ID No 14918; 322pp; English.
XX
CC   The present invention relates to novel single exon nucleic acid probes
CC   (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for measuring human gene expression in
CC   a human breast sample, where the probe hybridises at high stringency to a
CC   nucleic acid expressed in the human breast. The probes are useful for
CC   predicting, diagnosing, grading, staging, monitoring and prognosing
CC   diseases of the human breast, particularly those diseases with polygenic
CC   aetiology. The diseases include: breast cancer, disorders of development,
CC   inflammatory diseases of the breast, fibrocystic changes, proliferative
CC   breast disease and non-carcinoma tumours.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   68 AA;

Alignment Scores:
Pred. No.:              7.91e-28        Length:         68
Score:                  366.00          Matches:        68
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            13.12%          Indels:         0
DB:                     22              Gaps:           0

US-09-745-506-74 (1-1553) x AAM06178 (1-68)

Qy        395 ATGGAGGAGGTGCTGCAAAAGAAGGCAGACCTCATTCTCTCCTACCATCCGCCTATCTTC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGluGluValLeuGlnLysLysAlaAspLeuIleLeuSerTyrHisProProIlePhe 20

Qy        455 CGACCCATGAAGCGCATAACCTGGAACACATGGAAGGAGCGCCTGGTGATCCGGGCTCTG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         21 ArgProMetLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeu 40

Qy        515 GAGAACAGAGTCGGTATCTACTCTCCTCATACAGCCTATGATGCTGCGCCCCAGGGCGTC 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal 60

Qy        575 AACAACTGGTTGGCTAAAGGGCTT 598
              ||||||||||||||||||||||||
Db         61 AsnAsnTrpLeuAlaLysGlyLeu 68
```

Search completed: August 22, 2003, 13:59:08
Job time : 112 secs